

WHAT IS CLAIMED IS:

1. A method for separating a polypeptide species from a sample solution containing a plurality of polypeptide species and identifying said polypeptide species, the method comprising electrophoresing said sample solution containing a plurality of polypeptide species in a capillary electrophoresis device to separate and elute polypeptide species thereby resolving said protein species based on at least one first biophysical parameter which discriminates protein species; and obtaining, by mass spectrographic fragmentation of eluted polypeptide species, a polypeptide sequence tag ("PST") identifying at least one resolved protein species.
2. The method of claim 1, wherein the method further comprises electrophoresing polypeptide species eluted from said capillary electrophoresis device in a second capillary electrophoresis device to separate and elute polypeptide species thereby resolving said protein species based on at least one second biophysical parameter which discriminates protein species, prior to performing mass spectrographic fragmentation on the polypeptide species thereby obtained.
3. The method of claim 1, wherein the capillary electrophoresis device is a capillary isoelectric focusing (CIEF) device, a capillary zone electrophoresis device (CZE), or a capillary gel electrophoresis device (CGE).
4. The method of claim 2, wherein the capillary electrophoresis device is a CIEF device and the second capillary electrophoresis device is either a CZE device or a CGE device.
5. The method of claim 2, wherein the capillary electrophoresis device is a CZE device and the second capillary electrophoresis device is either a CIEF device or a CGE device.

6. The method of claim 2, wherein the capillary electrophoresis device is a CGE device and the second capillary electrophoresis device is either a CIEF device or a CZE device.
7. The method of claim 2, wherein the method further comprises electrophoresing polypeptide species eluted from said second capillary electrophoresis device in a third capillary electrophoresis device to separate and elute polypeptide species thereby resolving said protein species based on at least one third biophysical parameter which discriminates protein species, prior to performing mass spectrographic fragmentation on the polypeptide species thereby obtained.
8. The method of claim 7, wherein the the capillary electrophoresis device is a CIEF device and the second capillary electrophoresis device is either a CZE device and the third capillary electrophoresis device is a CGE device.
9. The method of claim 1, wherein the sample solution containing a plurality of polypeptide species comprises labeled polypeptide species.
10. The method of claims 1, 2, and 7 wherein the polypeptide species are labeled after capillary electrophoresis and prior to mass spectroscopy.
11. The method of claims 9 and 10, wherein the label comprises a detectable moiety.
12. The method of claims 9 and 10, wherein the label comprises an ion mass signature component.
13. The method of claims 9 and 10, wherein the label comprises an ion mass signature component and a detectable moiety.
14. A method for identifying a high-resolution protein expression fingerprint for a cell type, tissue, or pathological sample, comprising obtaining a protein-containing extract of a cellular sample and electrophoresing said extract with a first capillary electrophoresis

apparatus, eluting protein-containing fractions therefrom, electrophoresing said protein containing fractions on a second capillary electrophoresis apparatus, or plurality thereof in parallel, and identifying the species of proteins by fragmentation mass spectroscopy sequencing to obtain PSTs for a plurality of protein species, and compiling a dataset or fingerprint record containing the collection of PSTs obtained thereby.

15. The method of claim 14, comprising quantitative detection of protein species and compiling a dataset wherein the relative abundance and/or absolute amount of a plurality of protein species eluted from said second capillary electrophoresis are cross-tabulated with the PST identification.
16. A protein expression fingerprint comprising an array of at least 100 protein species each having a unique identifier cross-tabulated with quantitative data indicating relative and/or absolute abundance of each species in a sample.
20. A protein expression fingerprint comprising an array of at least 100 protein species each having a PST cross-tabulated with a separation coordinate.
20. A protein expression fingerprint comprising an array of at least 100 protein species each having a PST obtained by the method of claim 1.
20. A method for producing a computer database comprising a computer and software for storing in computer-retrievable form a collection of protein expression fingerprint records cross-tabulated with data specifying the source of the protein-containing sample from which each protein expression fingerprint record was obtained.
20. The method of claim 19, wherein at least one of the sources is from a tissue sample known to be free of pathological disorders.
21. The method of claim 19, wherein at least one of the sources is a known pathological tissue specimen.